RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/530,217
Source: PCT
Date Processed by STIC: 4-12-05

ENTERED

PCT

RAW SEQUENCE LISTING DATE: 04/12/2005
PATENT APPLICATION: **US/10/530,217** TIME: 14:05:35

Input Set : **A:\082368-003910US.txt**
Output Set: **N:\CRF4\04122005\J530217.raw**

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      4 <110> APPLICANT: Nakamura, Yusuke
      5       Katagiri, Toyomasa
      7 <120> TITLE OF INVENTION: GENES AND POLYPEPTIDES RELATING TO HUMAN
      8       MYELOID LEUKEMIA
     10 <130> FILE REFERENCE: 082368-003910US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/530,217
C--> 12 <141> CURRENT FILING DATE: 2005-03-30
     12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09589
     13 <151> PRIOR FILING DATE: 2003-07-29
     15 <150> PRIOR APPLICATION NUMBER: US 60/414,867
     16 <151> PRIOR FILING DATE: 2002-09-30
     18 <160> NUMBER OF SEQ ID NOS: 16
     20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     24 <212> TYPE: DNA
     25 <213> ORGANISM: Artificial Sequence
     27 <220> FEATURE:
     28 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
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     31 <400> SEQUENCE: 1
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     36 <212> TYPE: DNA
     37 <213> ORGANISM: Artificial Sequence
     39 <220> FEATURE:
     40 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
     41       RT-PCR
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     49 <212> TYPE: DNA
     50 <213> ORGANISM: Artificial Sequence
     52 <220> FEATURE:
     53 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
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     59 <210> SEQ ID NO: 4
     60 <211> LENGTH: 23
     61 <212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
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<213> ORGANISM: Artificial Sequence
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<210> SEQ ID NO: 9
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 9
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<213> ORGANISM: Artificial Sequence
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ggggtacccc agtggagctg agcgtccag 29
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<211> LENGTH: 18
<212> TYPE: DNA
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<220> FEATURE:
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ctgtgtgatg gacgtctg 18
<210> SEQ ID NO: 12
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: S-oligonucleotide sequence for antisense
<400> SEQUENCE: 12
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<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<210> SEQ ID NO: 14
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Target sequence for siRNA
<400> SEQUENCE: 14
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<211> LENGTH: 2958
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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200 ccccccagag acccccggcg gcggcagcct gccttgctct gccaggaacc atg agt    116
201                                                          Met Ser
202                                                           1
204 gag gcc cgc agg gac agc acg agc agc ctg cag cgc aag aag cca ccc   164
205 Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
206          5                  10                  15
208 tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag   212
209 Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
210      20                  25                  30
212 ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg   260
213 Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
214  35                  40                  45                  50
216 agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc   308
217 Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
218                  55                  60                  65
220 cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc   356
221 Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
222              70                  75                  80
224 agg ggg acc gcc gac tgg ttt gga gtg agc aag gac agt gac agc acc   404
225 Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
226          85                  90                  95
228 cag aaa tgg cag cgc aag agc atc cgt cac tgc agc cag cgc tac ggg   452
229 Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
230     100                 105                 110
232 aag ctg aag ccc cag gtc ctc cgg gag ctg gac ctg ccc agc cag gac   500
233 Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
234 115                 120                 125                 130
236 aac gtg tcg ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg   548
237 Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
238                 135                 140                 145
240 cca tgc cag ctg ggc atg cag aag atc ata gac ccc ctg gcc cgt ggc   596
241 Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
242             150                 155                 160
244 cgt gcc ttc cgt gtg gca gat gac act gcg gaa ggc ctg agt gcc cca   644
245 Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser Ala Pro
246         165                 170                 175
248 cac act ccc gtc acg ccg ggt gct gcc tcc ctc tgc tcc ttc tcc agc   692
249 His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe Ser Ser
250     180                 185                 190
252 tcc cgc tca ggt ttc cac cgg ctc ccg cgg cgg cgc aag cga gag tcg   740
253 Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg Glu Ser
254 195                 200                 205                 210
256 gtg gcc aag atg agc ttc cgg gcg gcc gca gcg ctg atg aaa ggc cgc   788
257 Val Ala Lys Met Ser Phe Arg Ala Ala Ala Ala Leu Met Lys Gly Arg
258                 215                 220                 225
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260 tcc gtt agg gat ggc acc ttt cgc cgg gca cgg cgt cga agc ttc act   836
261 Ser Val Arg Asp Gly Thr Phe Arg Arg Ala Arg Arg Arg Ser Phe Thr
262             230                 235                 240
264 cca gct agc ttt ctg gag gag gac aca act gat ttc ccc gat gag ctg   884
265 Pro Ala Ser Phe Leu Glu Glu Asp Thr Thr Asp Phe Pro Asp Glu Leu
266         245                 250                 255
268 gac aca tcc ttc ttt gcc cgg gaa ggt atc ctc cat gaa gag ctg tcc   932
269 Asp Thr Ser Phe Phe Ala Arg Glu Gly Ile Leu His Glu Glu Leu Ser
270     260                 265                 270
272 aca tac ccg gat gaa gtt ttc gag tcc cca tcg gag gca gcg cta aag   980
273 Thr Tyr Pro Asp Glu Val Phe Glu Ser Pro Ser Glu Ala Ala Leu Lys
274 275                 280                 285                 290
276 gac tgg gag aag gca ccg gag cag gcg gac ctc acc ggc ggg gcc ctg  1028
277 Asp Trp Glu Lys Ala Pro Glu Gln Ala Asp Leu Thr Gly Gly Ala Leu
278                 295                 300                 305
280 gac cgc agc gag ctt gag cgc agc cac ctg atg ctg ccc ttg gag cga  1076
281 Asp Arg Ser Glu Leu Glu Arg Ser His Leu Met Leu Pro Leu Glu Arg
282             310                 315                 320
284 ggc tgg cgg aag cag aag gag ggc gcc gca gcc ccg cag ccc aag gtg  1124
285 Gly Trp Arg Lys Gln Lys Glu Gly Ala Ala Ala Pro Gln Pro Lys Val
286         325                 330                 335
288 cgg ctc cga cag gag gtg gtg agc acc gcg ggg ccg cga cgg ggc cag  1172
289 Arg Leu Arg Gln Glu Val Val Ser Thr Ala Gly Pro Arg Arg Gly Gln
290     340                 345                 350
292 cgt atc gcg gtg ccg gtg cgc aag ctc ttc gcc cgg gag aag cgg ccg  1220
293 Arg Ile Ala Val Pro Val Arg Lys Leu Phe Ala Arg Glu Lys Arg Pro
294 355                 360                 365                 370
296 tat ggg ctg ggc atg gtg gga cgg ctc acc aac cgc acc tac cgc aag  1268
297 Tyr Gly Leu Gly Met Val Gly Arg Leu Thr Asn Arg Thr Tyr Arg Lys
298                 375                 380                 385
300 cgc atc gac agc ttc gtc aag cgc cag atc gag gac atg gac gac cac  1316
301 Arg Ile Asp Ser Phe Val Lys Arg Gln Ile Glu Asp Met Asp Asp His
302             390                 395                 400
304 agg ccc ttc ttc acc tac tgg ctt acc ttc gtg cac tcg ctc gtc acc  1364
305 Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu Val Thr
306         405                 410                 415
308 atc cta gcc gtg tgc atc tat ggc atc gcg ccc gtg ggc ttc tcg cag  1412
309 Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe Ser Gln
310     420                 425                 430
312 cat gag acg gtg gac tcg gtg ctg cgg aac cgc ggg gtc tac gag aac  1460
313 His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr Glu Asn
314 435                 440                 445                 450
316 gtc aag tac gtg cag cag gag aac ttc tgg atc ggg ccc agc tcg gag  1508
317 Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly Pro Ser Ser Glu
318                 455                 460                 465
320 gcc ctc atc cac ctg ggc gcc aag ttt tcg ccc tgc atg cgc cag gac  1556
321 Ala Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Met Arg Gln Asp
322             470                 475                 480
324 ccg cag gtg cac agc ttc att cgc tcg gcg cgc gag cgc gag aag cac  1604
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VERIFICATION SUMMARY DATE: 04/12/2005
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Output Set: **N:\CRF4\04122005\J530217.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date